GSK-3B Sequence

Met 1	Ser	Gly /	Arg	Pro 5	-	Thr _.	Thr	Ser	Phe 1		Glu	Ser	Cys	L y s 1!	_
Val	GIn	G1n 20		Ser	Ala	Phe		Ser 5	Met	Lys	Val	Ser 3		Asp	Lys
Asp	Gly	Ser I 35	-	Val	Thr	Thr	Val 4	_	Ala	Thr	Pro	Gly 4		Gly	Pro
Asp	Arg	Pro (Glu	Val	Ser	-	Thr 5	Asp	Thr	Lys	Val 6		Gly	Asn
G1y 65	Ser	Phe (Gly	Val	Va1 70	Tyr	Gln	Ala	Lys	Leu 75	Cys	Asp	Ser	Gly	G1u 80
Leu	Val	Ala 85		Lys	Lys	Val		G1n O	Asp	Lys	Arg		Lys 5	Asn	Arg
Glu	Leu	Gln 10		Met	Arg	Lys		Asp 05	His	Cys	Asn		Va1 10	Arg	Leu
Arg	Tyr	Phe 11		Tyr	Ser	Ser		G1u 20	Lys	Lys	Asp		Va1 25	Tyr	Leu
Asn	Leu	Val 13		Asp	Tyr	Val		Glu 35	Thr	Val	Tyr	•	Va1 40	Ala	Arg
His 145	Tyr	Ser	Arg	Ala	Lys 150	Gln	Thr	Leu	Pro	Va 1 155	Ile	Tyr	Val	Lys	Leu 160
Tyr	Met	Tyr (Leu	Phe	Arg		Leu 70	Ala	Tyr	Ile		Ser 75	Phe	Gly
Ile	Cys	His 18		Asp	Ile	Lys		G1n 85	Asn	Leu	Leu	_	Asp 90	Pro	Asp
Thr	Ala	Va 1		Lys	Leu	Cys	-	Phe 00	Gly	Ser	Ala		G1n 05	Leu	Val

Arg	G1y 210	Glu	Pro	Asn	Val	Ser 215	Tyr	Ile	Cys	Ser	Arg 220	Tyr	Tyr	Arg	Ala
Pro 225	Glu	Leu	Ile	Phe	G1y 230	Ala	Thr	Asp	Tyr	Thr 235	Ser	Ser	Ile	Asp	Va1 240
Trp	Ser	Ala	G1y	Cys 245	Val	Leu	Ala	Glu	Leu 250	Leu	Leu	Ġly	Gln	Pro 255	Ile
Phe	Pro	Gly	Asp 260	Ser	Gly	Val	Asp	G1n 265	Leu	Val	Glu	Ile	11e 270	Lys	Val .
Leu	Gly	Thr 275	Pro	Thr	Arg	Glu	G1n 280	Ile	Arg	Glu	Met	Asn 285	Pro	Asn	Tyr
Thr	G1u 290	Phe	Lys	Phe	Pro	61n 295	Ile	Lys	Ala	His	Pro 300	Trp	Thr	Lys	Val
Phe 305	Arg	Pro	Arg	Thr	Pro 310	Pro	Glu	Ala	Ile	Ala 315		Cys	Ser	Arg	Leu 320
Leu	Glu	Tyr	Thr	Pro 325	Thr	Ala	Arg	Leu	Thr 330	Pro	Leu	Glu	Ala	Cys 335	Ala
His	Ser	Phe	Phe 340	Asp	Glu	Leu	Arg	Asp 345	Pro	Asn	Val	Lys	His 350	Pro	Asn
Gly	Arg	Asp 355	Thr	Pro	Ala	Leu	Phe 360	Asn	Phe	Thr	Thr	G1n 365	Glu	Leu	Ser
Ser	Asn 370	Pro	Pro	Leu	Ala	Thr 375	Ile	Leu	Ile	Pro	Pro 380	His	Ala	Arg	Ile
G1n 385	Ala	Ala	Ala	Ser	Thr 390	Pro	Thr	Asn	Ala	Thr 395	Ala	Ala	Ser	Asp	Ala 400
Asn	Thr	Gly	Asp	Arg 405	Gly	Gln	Thr	Asn	Asn 410	Ala	Ala	Ser	Ala	Ser 415	Ala
Ser.	Asn	Ser	Thr 420												

Fig. 1B

GSK-3β 557 Construct Sequence Met Glu Tyr Met Pro Met Glu Gly Gly Gly

Met 1	Ser	Gly	Arg	Pro 5	•	Thr	Thr	Ser	Phe 1		Glu	Ser	Cys	Lys 1	_
Val	Gln	G1n 2	_	Ser	Ala	Phe		Ser 5	Met	Lys	Val	Ser 3	<u> </u>	Asp	Lys
Asp	Gly	Ser 3		Val	Thr	Thr	Val 4		Ala	Thr	Pro	Gly 4		Gly	Pro
Asp	Arg	Pro 5		Glu	Val	Ser	-	Thr 5	Asp	Thr	Lys	Va1 6	_	Gly	Asn
Gly 65	Ser	Phe	Gly	Val	Va1 70	Tyr	Gln	Ala	Lys	Leu 75	Cys	Asp	Ser	Gly	Glu 80
Leu	Val		Ile 5	Lys	Lyș	Val		Gln 0	Asp	Lys	Arg		Lys 5	Asn	Arg
Glu	Leu		Ile 00	Met	Arg	Lys		Asp 05	His	Cys	Asn		Va1 10	Arg	Leu
Arg	Tyr		Phe 15	Tyr	Ser	Ser	_	Glu 20	Lys	Lys	Asp		Va1 25	Tyr	Leu
Asn	Leu		Leu 30	Asp	Tyr	Val		G1u 35	Thr	Val	Tyr	_	Va1 40	Ala	Arg
His 145	Tyr	Ser	Arg	Ala	Lys 150	G1n	Thr	Leu	Pro	Va1 155	Ile	Tyr	Val	Lys	Leu 160
Tyr	Met		G1n 65	Leu	Phe	Arg		Leu 70	Ala	Tyr	Ile		Ser 75	Phe	Gly
Ile	Cys		Arg 80	Asp	Ile	Lys		G1n 85	Asn	Leu	Leu		Asp 90	Pro	Asp
Thr	Ala		Leu 95	Lys	Leu	Cys	•	Phe 00	Gly	Ser	Ala	-	G1n 05	Leu	Val
Arg	Gly		Pro 10	Asn	Val		2	15	Cys		Arg		Tyr 20	Arg	Ala
						H		ľ		/					

Fig. 2A

Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val 225 230 235 240	
Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile 245 250 255	1
Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val 260 265 270	•
Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr 275 280 285	
Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val 290 295 300	
Phe Arg Pro Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu 305 310 315 320	
Leu Glu Tyr Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala 325 330 335	
His Ser Phe Phe Asp Glu Leu Arg Asp Pro Asn Val Lys His Pro Asn 340 345 350	
Gly Arg Asp Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser 355 360 365	
Ser Asn Pro Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile 370 375 380	

GSK-3ß 580 Construct Sequence Het Glu Tyr Het Pro Het Glu Gly Gly Gly

G	y Se	er Lys Va 35	al Th	ir Th	ır Va	17 Val Al 40	la Tr	ar Pr	ro Gi	ly G1 4!		y Pr	0
sp	Arg	Pro G1n 50	Glu	Val	Ser	Tyr Thr 55	Asp	Thr	Lys	Va1 60		Gly	Asn
ily 65	Ser	Phe Gly	Val	Va1 70	Tyr	Gln Ala	Lys	Leu 75	Cys.	Asp	Ser	Gly	G1u 80
.eu	Val	Ala Ile 85	Lys	Lys	Val	Leu Gln 90	Asp	Lys	Arg		Lys 5	Asn	Arg
ilu	Leu	Gln Ile 100	Met	Arg	Lys	Leu Asp 105	His	Cys	Asn	Ile 11		Arg	Leu
irg	Tyr	Phe Phe 115	Tyr	Ser	Ser	Gly Glu 120	Lys	Lys	Asp	Glu 12		Tyr	Leu
lsn	Leu	Val Leu 130	Asp	Tyr	Val	Pro Glu 135	Thr	Val	Tyr	Arg 14		Ala	Arg
tis 145	Tyr	Ser Arg	Ala	Lys 150	Gln	Thr Leu	Pro	Va1 155	Ile	Tyr	Val	Lys	Leu 160
yr	Met	Tyr Gln 165	Leu	Phe	Arg	Ser Leu 170	Ala	Tyr	Ile	His 17		Phe	Gly
lle	Cys	His Arg 180	Asp	Ile	Lys	Pro Gln 185	Asn	Leu	Leu	Leu 19	•	Pro	Asp
Thr	Ala	Val Leu 195	Lys	Leu	Cys	Asp Phe 200	Gly	Ser	Ala	Lys 20		Leu	Val
\rg	Gly	Glu Pro 210	Asn	Val	Ser	Tyr Ile 215	Cys	Ser	Arg	Tyr 22	_	Arg	Ala
Pro 225		Leu Ile	Phe	G1y 230	Ala	Thr Asp	Tyr	Thr 235	Ser	Ser	Ile	Asp	Va1 240

Trp Ser Ala Gl	y Cys Val Le 245	eu Ala Glu Leu 250	Leu Leu Gly Gln	Pro Ile 255
Phe Pro Gly As 26		al Asp Gin Leu 265	Val Glu Ile Ile 270	Lys Val
Leu Gly Thr Pr 275	o Thr Arg G1	lu Gln Ile Arg 280	Glu Met Asn Pro 285	Asn Tyr
Thr Glu Phe Ly 290	s Phe Pro G1 29	•	His Pro Trp Thr 300	Lys Val
Phe Arg Pro Ar 305	g Thr Pro Pr 310		Ala Leu Cys Ser 315	Arg Leu 320
Leu Glu Tyr Th	r Pro Thr Al 325	la Arg Leu Thr 330	Pro Leu Glu Ala	Cys Ala 335
His Ser Phe Ph 34	•	eu Arg Asp Pro 345	Asn Val Lys His 350	Pro Asn
Gly Arg Asp Th	r Pro Ala Le	eu Phe Asn Phe 360	Thr Thr Gln Glu 365	Leu Ser
Ser Asn Pro Pr 370	o Leu Ala Th 37		Pro Pro His Ala 380	Arg Ile

Human GSK3 α

MSGGGPSGGG	PGGSGRARTS	SFAEPGGGGG	GGGGGPGGSA	SGPGGTGGGK
1				50
ASVGAMGGGV	GASSSGGGPG	GSGGGGGGP	GAGTSFPPPG	VKLGRDSGKV
51				100
TTVVATLGQG	PERSQEVAYT	DIKVIGNGSF	GVVYQARLAE	TRELVAIKKV
101				150
LQDKRFKNRE	LQIMRKLDHC	NIVRLRYFFY	SSGEKKDELY	LNLVLEYVPE
151	-			200
TVYRVARHFT	KAKLTIPILY	VKVYMYQLFR	SLAYIHSQGV	CHRDIKPONL
201			-	250
LVDPDTAVLK	LCDFGSAKQL	VRGEPNVSYI	CSRYYRAPEL	IFGATDYTSS
251				300
IDVWSAGCVL	AELLLGQPIF	PGDSGVDQLV	EIIKVLGTPT	REQIREMNPN
301				350
YTEFKFPQIK	AHPWTKVFKS	RTPPEAIALC	SSLLEYTPSS	RLSPLEACAH
351		•		400
SFFDELRCLG	TQLPNNRPLP	PLFNFSAGEL	SIQPSLNAIL	IPPHLRSPAG
401				450
TTTLTPSSQA	LTETPTSSDW	QSTDATPTLT	NSS	
451			483	

Human GSK 3α

MSGGGPSGGG	PGGSGRARTS	SFAEPGGGG	GGGGGPGGSA	SGPGGTGGGK
1				50
ASVGAMGGGV	GASSSGGGPG	GSGGGGGGP	GAGTSFPPPG	VKLGRDSGKV
51				100
TTVVATLGQG	PERSQEVAYT	DIKVIGNGSF	GVVYQARLAE	TRELVAIKKY
101		,		150
LQDKRFKNRE	LQIMRKLDHC	NIVRLRYFFY	SSGEKKDELY	LNLVLEYVPE
151				200
TYYRVARHFT	KAKLTIPILY	VKVYMYQLFR	SLAYIHSQGV	CHRDIKPONL
201				250
LVDPDTAVLK	LCDFGSAKQL	VRGEPNVSYI	CSRYYRAPEL	IFGATDYTSS
251		=		300
IDVWSAGCVL	AELLLGQPIF	PGDSGVDQLV	EIIKVLGTPT	REQIREMNPN
301				350
YTEFKFPQIK	AHPWTKVFKS	RTPPEAIALC	SSLLEYTPSS	RLSPLEACAH
351				400
SFFDELRCLG	TQLPNNRPLP	PLFNFSAGEL	SIQPSLNAIL	IPPHLRS
401				

Human GSK3a

				SGKV
				100
TTVVATLGQG	PERSQEVAYT	DIKVIGNGSF	GVVYQARLAE	TRELVAIKKY
101				150
LQDKRFKNRE	LQIMRKLDHC	NIVRLRYFFY	SSGEKKDELY	LNLVLEYVPE
151				200
TVYRVARHFT	KAKLTIPILY	VKVYMYQLFR	SLAYIHSQGV	CHRDIKPQNL
201				250
LVDPDTAVLK	LCDFGSAKQL	VRGEPNVSYI	CSRYYRAPEL	IFGATDYTSS
251				300
IDVWSAGCVL	AELLLGQPIF	PGDSGVDQLV	EIIKVLGTPT	REQIREMNPN
301		•		350
YTEFKFPQIK	AHPWTKVFKS	RTPPEAIALC	SSLLEYTPSS	RLSPLEACAH
351				400
SFFDELRCLG	TQLPNNRPLP.	PLFNFSAGEL	SIQPSLNAIL	IPPHLRSPAG
401	•			450
TTTLTPSSQA	LTETPTSSDW	QSTDATPTLT	NSS	
451			483	

Human GSK 3α

				SGKV
				100
TTVVATLGQG	PERSQEVAYT	DIKVIGNGSF	GVVYQARLAE	TRELVAIKKY
101			-	150
LQDKRFKNRE	LQIMRKLDHC	NIVRLRYFFY	SSGEKKDELY	LNLVLEYVPE
151				200
TVYRVARHFT	KAKLTIPILY	VKVYMYQLFR	SLAYIHSQGV	CHRDIKPQNL
201				250
LVDPDTAVLK	LCDFGSAKQL	VRGEPNVSYI	CSRYYRAPEL	IFGATDYTSS
251				300
IDVWSAGCVL	AELLLGQPIF	PGDSGVDQLV	EIIKVLGTPT	REQIREMNPN
301				350
YTEFKFPQIK	AHPWTKVFKS	RTPPEAIALC	SSLLEYTPSS	RLSPLEACAH
351				400
SFFDELRCLG	TQLPNNRPLP	PLFNFSAGEL	SIQPSLNAIL	IPPHLRS
401				